

SEQUENCE LISTING

<110> Croteau, Rodney et al.

<120> Transacylases of the Paclitaxel Biosynthetic Pathway

<130> 53679

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<150> 09/411,145

<151> 1999-09-30

<160> 58

<170> PatentIn Ver. 2.0

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<211> 920

<212> DNA

<213> Taxus cuspidata

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<213> Taxus cuspidata

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Glu Ala Met Ala Asp Asn Glu Leu Ser Val Leu Gly Asp Phe Asp Asp
    35                      40          45

Ser Asn Pro Ser Phe Gln Gln Leu Leu Phe Ser Leu Pro Leu Asp Thr
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Asn Phe Lys Asp Leu Ser Leu Leu Val Val Gln Val Thr Arg Phe Thr
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 115 120 125
 Lys Leu Asp Asp Pro Lys Tyr Leu Gln Phe Phe His Phe Glu Phe Leu
 130 135 140
 Arg Ala Pro Ser Ile Val Glu Lys Ile Val Gln Thr Tyr Phe Ile Ile
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 Asp Leu Glu Thr Ile Asn Tyr Ile Lys Gln Ser Val Met Glu Glu Cys
 165 170 175
 Lys Glu Phe Cys Ser Ser Phe Glu Val Ala Ser Ala Met Thr Trp Ile
 180 185 190
 Ala Arg Thr Arg Ala Phe Gln Ile Pro Glu Ser Glu Tyr Val Lys Ile
 195 200 205
 Leu Phe Gly Met Asp Met Arg Asn Ser Phe Asn Pro Pro Leu Pro Ser
 210 215 220
 Gly Tyr Tyr Gly Asn Ser Ile Gly Thr Ala Cys Ala Val Asp Asn Val
 225 230 235 240
 Gln Asp Leu Leu Ser Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys
 245 250 255
 Lys Ser Lys Val Ser Leu Asn Asp Asn Phe Lys Ser Arg Ala Val Val
 260 265 270
 Lys Pro Ser Glu Leu Asp Val Asn Met Asn His Glu Asn Val Val Ala
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<213> Taxus cuspidata

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Glu Ala Met Ala Asp Asn Asp Leu Ser Val Leu Gln Asp Phe Asn Glu
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Tyr Asp Pro Ser Phe Gln Gln Leu Val Phe Tyr Leu Pro Glu Asp Val
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Asn Ile Glu Asp Leu His Leu Leu Thr Val Gln Val Thr Arg Phe Thr
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Cys Gly Gly Phe Val Val Gly Thr Arg Phe His His Ser Val Ser Asp
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Gly Lys Gly Ile Gly Gln Leu Leu Lys Gly Met Gly Glu Met Ala Arg
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Gly Glu Phe Lys Pro Ser Leu Glu Pro Ile Trp Asn Arg Glu Met Val
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Lys Pro Glu Asp Ile Met Tyr Leu Gln Phe Asp His Phe Asp Phe Ile
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His Pro Pro Leu Asn Leu Glu Lys Ser Ile Gln Ala Ser Met Val Ile
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Ser Leu Glu Arg Ile Asn Tyr Ile Lys Arg Cys Met Met Glu Glu Cys
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Lys Glu Phe Phe Ser Ala Phe Glu Val Val Val Ala Leu Ile Trp Leu
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Ala Arg Thr Lys Ser Phe Arg Ile Pro Pro Asn Glu Tyr Val Lys Ile
195 200 205

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Ile Phe Pro Ile Asp Met Arg Asn Ser Phe Asp Ser Pro Leu Pro Lys
210 215 220

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Gly Tyr Tyr Gly Asn Ala Ile Gly Asn Ala Cys Ala Met Asp Asn Val
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Lys Asp Leu Leu Asn Gly Ser Leu Leu Tyr Ala Leu Met Leu Ile Lys

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245 250 255

Lys Ser Lys Phe Ala Leu Asn Glu Asn Phe Lys Ser Arg Ile Leu Thr
 260 265 270

Lys Pro Ser Ala Leu Asp Ala Asn Met Lys His Glu Asn Val Val Gly
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Gly Lys
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 <213> *Taxus cuspidata*

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      20           25           30

Asp Ser Asp Leu Ser Val Leu Thr Asp Leu Asp Asp Tyr Lys Pro Ser
      35           40           45

Phe Gln Gln Leu Ile Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp
      50           55           60

Leu His Leu Leu Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65           70           75           80

Val Val Gly Ala Asn Val Tyr Ser Ser Val Cys Asp Ala Lys Gly Phe
      85           90           95
  
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Gly Gln Phe Leu Gln Gly Met Ala Glu Met Ala Arg Gly Glu Val Lys
 100 105 110
 Pro Ser Ile Glu Pro Ile Trp Asn Arg Glu Leu Val Lys Pro Glu His
 115 120 125
 Cys Met Pro Phe Arg Met Ser His Leu Gln Ile Ile His Ala Pro Leu
 130 135 140
 Ile Glu Glu Lys Phe Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile
 145 150 155 160
 Ile Asn His Ile Arg Gln Arg Ile Met Glu Glu Cys Lys Glu Ser Phe
 165 170 175
 Ser Ser Phe Glu Ile Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys
 180 185 190
 Ala Phe Gln Ile Pro His Ser Glu Asn Val Lys Leu Leu Phe Ala Met
 195 200 205
 Asp Leu Arg Arg Ser Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Phe Gly Ile Ala Cys Ala Met Asp Asn Val His Asp Leu Leu
 225 230 235 240
 Ser Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Phe
 245 250 255
 Ser Leu His Lys Glu Leu Asn Ser Lys Thr Val Met Ser Pro Ser Val
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<213> *Taxus cuspidata*

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<213> Taxus cuspidata

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 35 40 45

Phe Gln Gln Leu Leu Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp
 50 55 60

Leu His Leu Leu Ile Val Gln Val Thr His Phe Thr Cys Gly Asp Phe
 65 70 75 80

Val Val Gly Ala Asn Val Tyr Gly Ser Val Cys Asp Gly Lys Gly Phe
 85 90 95

Gly Gln Phe Leu Gln Gly Met Ala Glu Met Ala Arg Gly Glu Val Lys
 100 105 110

Pro Ser Ile Glu Pro Ile Trp Asn Arg Glu Leu Val Lys Pro Glu Asp
 115 120 125

Leu Met Ala Leu His Val Asp His Leu Arg Ile Ile His Thr Pro Leu
 130 135 140

Ile Glu Glu Lys Phe Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile
 145 150 155 160

Ile Asn His Ile Arg Arg Cys Ile Met Glu Glu Cys Lys Glu Ser Phe
 165 170 175

Ser Ser Phe Glu Ile Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys
 180 185 190

Ala Phe Arg Ile Pro His Ser Glu Asn Val Lys Ile Leu Phe Ala Met
 195 200 205

Asp Val Arg Arg Ser Phe Lys Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220

Asn Ala Tyr Gly Ile Ala Cys Ala Met Asp Asn Val Gln Asp Leu Leu
 225 230 235 240

Ser Gly Ser Leu Leu His Ala Ile Met Ile Ile Lys Lys Ser Lys Phe
 245 250 255

Ser Leu His Lys Lys Ile Asn Ser Lys Thr Val Met Ser Pro Ser Pro
 260 265 270

Leu Asp Val Asn Met Lys Phe Glu Asn Val Val Ser Ile Thr Asp Trp

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280

285

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<210> 9

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<212> DNA

<213> Taxus cuspidata

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<213> Taxus cuspidata

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      20          25          30

Asp Asn Asp Leu Ser Ala Val Arg Asp Leu Asp Glu Tyr Asn Pro Leu
      35          40          45

Phe Arg Gln Leu Gln Ser Thr Leu Pro Leu Asp Thr Asp Cys Lys Asp
      50          55          60

Leu His Leu Met Thr Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65          70          75          80

Val Met Gly Thr Ser Val His Gln Ser Ile Cys Asp Gly Asn Gly Leu
      85          90          95

Gly Gln Phe Phe Lys Ser Met Ala Glu Met Val Arg Gly Glu Val Lys
      100          105          110

Pro Ser Ile Glu Pro Val Trp Asn Arg Glu Leu Val Lys Pro Glu Asp
      115          120          125

Tyr Ile His Leu Gln Leu Tyr Ile Gly Glu Phe Ile Arg Pro Pro Leu
      130          135          140

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Ala Phe Glu Lys Val Gly Gln Thr Ser Leu Ile Ile Ser Phe Glu Lys
145 150 155 160

Ile Asn His Ile Lys Arg Cys Ile Met Glu Glu Ser Lys Glu Ser Phe
165 170 175

Ser Ser Phe Glu Ile Val Thr Ala Leu Val Trp Leu Ala Arg Thr Arg
180 185 190

Ala Phe Gln Ile Pro His Asn Glu Asp Val Thr Leu Leu Leu Ala Met
195 200 205

Asp Ala Arg Arg Ser Phe Asp Pro Pro Ile Pro Lys Gly Tyr Tyr Gly
210 215 220

Asn Val Ile Gly Thr Ala Cys Ala Thr Asn Asn Val His Asn Leu Leu
225 230 235 240

Ser Gly Ser Leu Leu His Ala Leu Thr Ile Ile Lys Lys Ser Met Ser
245 250 255

Ser Phe Tyr Glu Asn Ile Thr Ser Arg Val Leu Val Asn Pro Ser Thr
260 265 270

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290 295 300

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<213> *Taxus cuspidata*

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<213> *Taxus cuspidata*

<400> 12

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Leu	Glu	Gln	Leu	Leu	Phe	Cys	Leu	Pro	Pro	Asp	Thr	Asp	Ile	Glu	Asp	50	55	60	
Ile	His	Pro	Leu	Val	Val	Gln	Val	Thr	Arg	Phe	Thr	Cys	Gly	Gly	Phe	65	70	75	80
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Pro	Ser	Ser	Glu	Pro	Ile	Trp	Lys	Arg	Glu	Leu	Leu	Lys	Pro	Glu	Asp	115	120	125	
Pro	Leu	Tyr	Arg	Phe	Gln	Tyr	Tyr	His	Phe	Gln	Leu	Ile	Cys	Pro	Pro	130	135	140	
Ser	Thr	Phe	Gly	Lys	Ile	Val	Gln	Gly	Ser	Leu	Val	Ile	Thr	Ser	Glu	145	150	155	160
Thr	Ile	Asn	Cys	Ile	Lys	Gln	Cys	Leu	Arg	Glu	Glu	Ser	Lys	Glu	Phe	165	170	175	
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Arg	Ala	Leu	Gln	Ile	Pro	His	Ser	Glu	Asn	Val	Lys	Leu	Ile	Phe	Ala	195	200	205	
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Gly	Asn	Phe	Val	Gly	Thr	Val	Cys	Ala	Met	Asp	Asn	Val	Lys	Asp	Leu	225	230	235	240
Leu	Ser	Gly	Ser	Leu	Leu	Arg	Val	Val	Arg	Ile	Ile	Lys	Lys	Ala	Lys	245	250	255	
Val	Ser	Leu	Asn	Glu	His	Phe	Thr	Ser	Thr	Ile	Val	Thr	Pro	Arg	Ser	260	265	270	
Gly	Ser	Asp	Glu	Ser	Ile	Asn	Tyr	Glu	Asn	Ile	Val	Gly	Phe	Gly	Asp	275	280	285	
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<210> 13
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<213> Taxus cuspidata

<400> 13

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<210> 14

<211> 322

<212> PRT

<213> Taxus cuspidata

<400> 14

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Phe Tyr Pro Phe Ala Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu
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Glu Val Glu Cys Thr Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala
              20              25              30

Asp Ser Asp Leu Ser Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser
      35              40              45

Phe Gln Gln Leu Ile Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp
      50              55              60

Leu His Leu Leu Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65              70              75              80

Val Val Gly Ala Asn Val Tyr Gly Ser Thr Cys Asp Ala Lys Gly Phe
              85              90              95

Gly Gln Phe Leu Gln Gly Met Ala Glu Met Ala Arg Gly Glu Val Lys
      100              105              110

Pro Ser Ile Glu Pro Ile Trp Asn Lys Arg Thr Gly Glu Ala Arg Arg
      115              120              125

Glu Val Lys Pro Ser Ile Glu Pro Ile Trp Asn Lys Arg Thr Gly Glu
      130              135              140

Ala Arg Arg Leu Tyr Ala Leu Ser Gly Met Ser His Leu Gln Ile Ile
      145              150              155              160

His Ala Pro Val Ile Glu Glu Lys Phe Val Gln Thr Ser Leu Val Ile
              165              170              175

Asn Phe Glu Ile Ile Asn His Ile Arg Arg Arg Ile Met Glu Glu Cys

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180 185 190

Lys Glu Ser Leu Ser Ser Phe Glu Ile Val Ala Ala Leu Val Trp Leu
195 200 205

Ala Lys Ile Lys Ala Phe Gln Ile Pro His Ser Glu Asn Val Lys Leu
210 215 220

Leu Phe Ala Met Asp Leu Arg Arg Ser Phe Asn Pro Pro Leu Pro His
225 230 235 240

Gly Tyr Tyr Gly Asn Ala Phe Gly Ile Ala Cys Ala Met Asp Asn Val
245 250 255

His Asp Leu Leu Ser Gly Ser Leu Leu Arg Thr Ile Met Ile Ile Lys
260 265 270

Lys Ser Lys Phe Ser Leu His Lys Glu Leu Asn Ser Lys Thr Val Met
275 280 285

Ser Ser Ser Val Val Asp Val Asn Thr Lys Phe Glu Asp Val Val Ser
290 295 300

Ile Ser Asp Trp Arg His Ser Ile Tyr Tyr Glu Val Asp Phe Gly Trp
305 310 315 320

Gly Lys

<210> 15
<211> 908
<212> DNA
<213> Taxus cuspidata

<400> 15
ttttaccggt ttgcggggcg tctcagaaat aaagaaaatg gggatctgga agtggagtgt 60
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gatttgatg ctcataatcc ttcatttcac cagctttctg tttcacctcc agtggattct 180
gatattgagg gcctccatct tgcagctctt caggtaactc gttttacatg tgggggtttt 240
gttctaggag taagtgtgaa ccaaagtgtg tgcgatggaa aaggattggg aaattttctt 300
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agagaaatgg taaagtttga agactataca cgctccaat tttatcacca tgaattcata 420
caaccacctt taatagatga gaaaattggt caaaaatctc ttgttataaa cttggagaca 480
ataaatatta tcaaacgatg tattatggaa gaatatataa aattttttctc tacattcgaa 540
atcgtagcag caatggtttg gctagcaaga acaaaagctt tcaaaattcc acatagtga 600
aatgcagagc ttctctttac aatggatatg agggaatcat ttaatcccc tcttccaaag 660
ggatactatg gtaatgttat gggtatagta tgtgcattgg ataatgtcaa acacctatta 720
agtggatcta ttttgcgtgc tgcaatgggt atacagaaat caagggtttt ctttacagag 780
aatttcgggt taagatctat gacacaacca tctgcattga ctgtgaagat caagcacaaa 840
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ggtaaacc 908

<210> 16
<211> 302
<212> PRT
<213> Taxus cuspidata

<400> 16
Phe Tyr Pro Phe Ala Gly Arg Leu Arg Asn Lys Glu Asn Gly Asp Leu
1 5 10 15

Glu Val Glu Cys Thr Gly Glu Gly Ala Val Phe Val Glu Ala Met Ala
 20 25 30
 Asp Thr Asp Leu Ser Ser Leu Gly Asp Leu Asp Ala His Asn Pro Ser
 35 40 45
 Phe His Gln Leu Ser Val Ser Pro Pro Val Asp Ser Asp Ile Glu Gly
 50 55 60
 Leu His Leu Ala Ala Leu Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
 65 70 75 80
 Val Leu Gly Val Ser Leu Asn Gln Ser Val Cys Asp Gly Lys Gly Leu
 85 90 95
 Gly Asn Phe Leu Lys Gly Val Ala Glu Met Val Arg Gly Lys Asp Lys
 100 105 110
 Pro Ser Ile Glu Pro Val Trp Asn Arg Glu Met Val Lys Phe Glu Asp
 115 120 125
 Tyr Thr Arg Leu Gln Phe Tyr His His Glu Phe Ile Gln Pro Pro Leu
 130 135 140
 Ile Asp Glu Lys Ile Val Gln Lys Ser Leu Val Ile Asn Leu Glu Thr
 145 150 155 160
 Ile Asn Ile Ile Lys Arg Cys Ile Met Glu Glu Tyr Thr Lys Phe Phe
 165 170 175
 Ser Thr Phe Glu Ile Val Ala Ala Met Val Trp Leu Ala Arg Thr Lys
 180 185 190
 Ala Phe Lys Ile Pro His Ser Glu Asn Ala Glu Leu Leu Phe Thr Met
 195 200 205
 Asp Met Arg Glu Ser Phe Asn Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220
 Asn Val Met Gly Ile Val Cys Ala Leu Asp Asn Val Lys His Leu Leu
 225 230 235 240
 Ser Gly Ser Ile Leu Arg Ala Ala Met Val Ile Gln Lys Ser Arg Phe
 245 250 255
 Phe Phe Thr Glu Asn Phe Arg Leu Arg Ser Met Thr Gln Pro Ser Ala
 260 265 270
 Leu Thr Val Lys Ile Lys His Lys Asn Val Val Ala Cys Ser Asp Trp
 275 280 285
 Arg Gln Tyr Gly Tyr Asp Glu Val Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 17

<211> 908

<212> DNA

<213> *Taxus cuspidata*

<400> 17

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ggttttgatt accacaatcc agcatttggg aagctacttt actcactacc actggatacc 180
cctattcacg acctccatcc tctggttgtt caggtaactc gttttacctg cgggggggtt 240
gttggtggat taagtttggg ccatactata tgtgatggac gtggtgcagg tcaatttctt 300
aaagcccctag cagaratggc gaggggagag gctaagccct cattggaacc aatatggaat 360
agagagtgtg tgaagcccga agaccttata cgcttgcaat tttatcactt tgaatcgatg 420
cgtccacctc caatagtgtg agaaatgggt caatcatcta ttattataaa tgctgagaca 480
ataagtaata tsaaacaata cattatggaa gaatgtaaaag aatcttggtc tgcatttgat 540
gtcgtaggag gattggcttg gctagccagg acaaaggctt ttcaaattcc acatacagag 600
aatgtgatgg ttatttttgc agtggatgag aggagatcat ttgatccacc acttccaaag 660
ggttactatg gtaatgtcgt tggtaatgca tgtgcattgg ataatgttca agacctctta 720
aatggatctc ttttgcgtgc tacaatgatt ataaagaaat caaaggatc tttaaaagag 780
aatataaggg caaaaacttt gacgatacca tctatagtag atgtgaatgt gaaacatgaa 840
aacatagtgt gattaggcga tttgagacga ctgggattta atgaagtgga cttcggctgg 900
ggsaagcc 908
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<210> 18

<211> 302

<212> PRT

<213> *Taxus cuspidata*

<400> 18

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Phe Tyr Pro Phe Ala Gly Arg Met Arg Asn Lys Gly Asp Gly Glu Leu
  1          5          10          15

Glu Val Asp Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Met Ala
      20          25          30

Asp Asp Asn Leu Ser Val Leu Gly Gly Phe Asp Tyr His Asn Pro Ala
      35          40          45

Phe Gly Lys Leu Leu Tyr Ser Leu Pro Leu Asp Thr Pro Ile His Asp
      50          55          60

Leu His Pro Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65          70          75          80

Val Val Gly Leu Ser Leu Asp His Thr Ile Cys Asp Gly Arg Gly Ala
      85          90          95

Gly Gln Phe Leu Lys Ala Leu Ala Glu Met Ala Arg Gly Glu Ala Lys
      100          105          110

Pro Ser Leu Glu Pro Ile Met Asn Arg Glu Leu Leu Lys Pro Glu Asp
      115          120          125

Leu Ile Arg Leu Gln Phe Tyr His Phe Glu Ser Met Arg Pro Pro Pro
      130          135          140

Ile Val Glu Glu Met Val Gln Ser Ser Ile Ile Ile Asn Ala Glu Thr
      145          150          155          160

Ile Ser Asn Xaa Lys Gln Tyr Ile Met Glu Glu Cys Lys Glu Ser Cys
      165          170          175

Ser Ala Phe Asp Val Val Gly Gly Leu Ala Met Leu Ala Arg Thr Lys
      180          185          190

Ala Phe Gln Ile Pro His Thr Glu Asn Val Met Val Ile Phe Ala Val
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195 200 205

Asp Ala Arg Arg Ser Phe Asp Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
210 ... 215 220

Asn Val Val Gly Asn Ala Cys Ala Leu Asp Asn Val Gln Asp Leu Leu
225 230 235 240

Asn Gly Ser Leu Leu Arg Ala Thr Met Ile Ile Lys Lys Ser Lys Val
245 250 255

Ser Leu Lys Glu Asn Ile Arg Ala Lys Thr Leu Thr Ile Pro Ser Ile
260 265 270

Val Asp Val Asn Val Lys His Glu Asn Ile Val Gly Leu Gly Asp Leu
275 280 285

Arg Arg Leu Gly Phe Asn Glu Val Asp Phe Gly Trp Gly Lys
290 295 300

<210> 19
<211> 911
<212> DNA
<213> *Taxus cuspidata*

<400> 19
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gatctggatg acctcaatcc atcatttcag cagttagttt tttggcatcc attggacact 180
gctattgagg atcttcatct tgtgattgtt caggtaacac gttttacatg tgggggcatt 240
gccgttggag tgactttgcc ccatagtgtg tgtgatggac gtggagcacc ccagtttgtt 300
acagcactgg cagaaatggc gaggggagag gttaagccct tattagaacc aatatggaat 360
agagaattgt tgaaccctga agaccctcta catctccagt taaatcaatt tgattcgata 420
tgcccacctc caatgctcga ggaattgggt caagcttctt ttgttataaa tgttgacacc 480
atagaatata tgaaacaatg tgttatggag gaatgtaatg atttttgttc gtcctttgaa 540
gtagtggcag cattggtttg gatagcaagg acaaaggctc ttcaaattcc acatactgag 600
aatgtgaagc ttctctttgc gatggatttg aggaaattat ttaatccccc acttccaaat 660
ggatattatg gtaatgccat tggtagtcca tatgcaatgg ataagtcca agacctctta 720
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aattattcga ggtcaagggt agttacaaac ccaaattcat tagatgtgaa caagaaatcc 840
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tggggcaagc c 911

<210> 20
<211> 303
<212> PRT
<213> *Taxus cuspidata*

<400> 20
Tyr Tyr Pro Leu Ala Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu
1 5 10 15
Glu Val Glu Cys Thr Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val
20 25 30
Glu Asp Thr Ile Ser Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser
35 40 45
Phe Gln Gln Leu Val Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp
50 55 60

Leu His Leu Val Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile
 65 70 75 80
 Ala Val Gly Val Thr Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala
 85 90 95
 Pro Gln Phe Val Thr Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys
 100 105 110
 Pro Leu Leu Glu Pro Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp
 115 120 125
 Pro Leu His Leu Gln Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro
 130 135 140
 Met Leu Glu Glu Leu Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr
 145 150 155 160
 Ile Glu Tyr Met Lys Gln Cys Val Met Glu Glu Cys Asn Asp Phe Cys
 165 170 175
 Ser Ser Phe Glu Val Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys
 180 185 190
 Ala Leu Gln Ile Pro His Thr Glu Asn Val Lys Leu Leu Phe Ala Met
 195 200 205
 Asp Leu Arg Lys Leu Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Ile Gly Thr Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu
 225 230 235 240
 Asn Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala
 245 250 255
 Asp Leu Lys Asp Asn Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Asn
 260 265 270
 Ser Leu Asp Val Asn Lys Lys Ser Asn Asn Ile Leu Ala Leu Ser Asp
 275 280 285
 Trp Arg Arg Leu Gly Phe Tyr Glu Ala Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 21
 <211> 911
 <212> DNA
 <213> *Taxus cuspidata*

<400> 21
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 gatctggatg acctcaatcc atcatttcag cagttagttt tttggcatcc attggacact 180
 gctattgagg atcttcatct tgtgattgtt caggtaacac gttttacatg tgggggcatt 240
 gccgttgag tgactttgcc ccatagtgtg tgtgatggac gtggagcacc ccagtttgtt 300
 acagcactgg cagaaatggc gaggggagag gttaagccct tattagaacc aatatggaat 360
 agagaattgt tgaaccctga agaccctcta catctccagt taaatcaatt tgattcgata 420
 tgccacctc caatgctcga ggaattgggt caagcttctt ttgttataaa tgttgacacc 480

atagaatata tgaaacaatg tggtatggag gaatgtaatg atttttgttc gtcctttgaa 540
 gtagtggcag cattggtttg gatagcaagg acaaaggctc ttcaaattcc acatactgag 600
 aatgtgaagc ttctctttgc gatggatttg aggaaattat ttaatccccc acttcctaat 660
 ggatattatg gtaatgccat tggtactgca tatgcaatgg ataatgtcca agacctctta 720
 aatggatctc ttttgcgtgc tataatgatt ataaaaaaag caaaggctga tttaaaagat 780
 aattattcga ggtcaagggt agttacaaac ccaaattcat tagatgtgaa caagaaatcc 840
 aacaacattc ttgcattgag tgactggagg cggttgggat tttatgaagc cgattttggc 900
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<210> 22

<211> 306

<212> PRT

<213> *Taxus cuspidata*

<400> 22

Tyr Tyr Pro Leu Ala Gly Arg Leu Glu Thr Cys Asp Gly Met Val Tyr
 1 5 10 15
 Ile Asp Cys Asn Asp Lys Gly Ala Glu Phe Ile Glu Ala Tyr Ala Ser
 20 25 30
 Pro Glu Leu Gly Val Ala Glu Ile Met Ala Asp Ser Phe Pro His Gln
 35 40 45
 Ile Phe Ala Phe Asn Gly Val Leu Asn Ile Asp Gly His Phe Met Pro
 50 55 60
 Leu Leu Ala Val Gln Ala Thr Lys Leu Lys Asp Gly Ile Ala Leu Ala
 65 70 75 80
 Ile Thr Val Asn His Ala Val Ala Asp Ala Thr Ser Val Trp His Phe
 85 90 95
 Ile Ser Ser Trp Ala Gln Leu Cys Lys Glu Pro Ser Asn Ile Pro Leu
 100 105 110
 Leu Pro Leu His Thr Arg Cys Phe Thr Thr Ile Ser Pro Ile Lys Leu
 115 120 125
 Asp Ile Gln Tyr Ser Ser Thr Thr Thr Glu Ser Ile Asp Asn Phe Phe
 130 135 140
 Pro Pro Pro Leu Thr Glu Lys Ile Phe His Phe Ser Gly Lys Thr Ile
 145 150 155 160
 Ser Arg Leu Lys Glu Glu Ala Met Glu Ala Cys Lys Asp Lys Ser Ile
 165 170 175
 Ser Ile Ser Ser Phe Gln Ala Leu Cys Gly His Leu Trp Gln Ser Ile
 180 185 190
 Thr Arg Ala Arg Gly Leu Ser Pro Ser Glu Pro Thr Thr Ile Lys Ile
 195 200 205
 Ala Val Asn Cys Arg Pro Arg Ile Val Pro Pro Leu Pro Asn Ser Tyr
 210 215 220
 Phe Gly Asn Ala Val Gln Val Val Asp Val Thr Met Thr Thr Glu Glu
 225 230 235 240
 Leu Leu Gly Asn Gly Gly Ala Cys Ala Ala Leu Ile Leu His Gln Lys

245

250

255

Ile Ser Ala His Gln Asp Thr Gln Ile Arg Ala Glu Leu Asp Lys Pro
 ... 260 265 270

Pro Lys Ile Val His Thr Asn Asn Leu Ile Pro Cys Asn Ile Ile Ala
 275 280 285

Met Ala Gly Ser Pro Arg Phe Pro Ile Tyr Asn Asn Asp Phe Gly Trp
 290 295 300

Gly Lys
 305

<210> 23

<211> 908

<212> DNA

<213> *Taxus cuspidata*

<400> 23

ttctaccogt tgcgggggcg gatcagacag aaagaaaatg aggaactgga agtggagtgc 60
 acagggggagg gtgcactgtt tgtggaagcc gtggtggaca atgatctttc agtcttgaaa 120
 gatttgatg cccaaaatgc atcttatgag cagttgctct tttcgcttcc gcccaataca 180
 caggttcagg acctccatcc tctgattctt caggttaactc gttttaaatg tggagggttt 240
 gttgtgggag ttggtttcca ccatagtata tgtgacgcac gaggaggaac tcaatttctt 300
 ctaggcctag cagatatggc aaggggagag actaagcctt tagtggaacc agtatggaat 360
 agagaactga taaaccctga agatctaattg cacctccaat ttcataagtt tggtttgata 420
 cgccaacctc taaaacttga tgaaatttgt caagcatctt ttactataaa ctcaaagata 480
 ataaattaca tcaaacaatg tggtatagaa gaatgtaatg aaattttctc tgcatttgaa 540
 gttgtagtag cattaacttg gatagcaagg acaaaggctt ttcaaattcc acatagttag 600
 aatgtgatga tgctcttttg aatggacgcg aggaaatatt ttaatcccc acttccaaag 660
 ggatattatg gtaatgccat tggtacttca tgtgtaattg aaaatgtaca agacctctta 720
 aatggatctc tttcgcgtgc tgtaatgatc acaaagaaat caaagggtccc ttttaattgag 780
 aatttaagggt caagaattgt ggcgaaccaa tctggagtag atgaggaaat taagcatgaa 840
 aacgtagttg gatttgagga ttggaggcga ttgggatttc atgaagtgga cttcgggctg 900
 ggcaagcc 908

<210> 24

<211> 302

<212> PRT

<213> *Taxus cuspidata*

<400> 24

Phe Tyr Pro Phe Ala Gly Arg Ile Arg Gln Lys Glu Asn Glu Glu Leu
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Glu Val Glu Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Val Val
 20 25 30

Asp Asn Asp Leu Ser Val Leu Lys Asp Leu Asp Ala Gln Asn Ala Ser
 35 40 45

Tyr Glu Gln Leu Leu Phe Ser Leu Pro Pro Asn Thr Gln Val Gln Asp
 50 55 60

Leu His Pro Leu Ile Leu Gln Val Thr Arg Phe Lys Cys Gly Gly Phe
 65 70 75 80

Val Val Gly Val Gly Phe His His Ser Ile Cys Asp Ala Arg Gly Gly
 85 90 95

Thr Gln Phe Leu Leu Gly Leu Ala Asp Met Ala Arg Gly Glu Thr Lys
 100 105 110
 Pro Leu Val Glu Pro Val Trp Asn Arg Glu Leu Ile Asn Pro Glu Asp
 115 120 125
 Leu Met His Leu Gln Phe His Lys Phe Gly Leu Ile Arg Gln Pro Leu
 130 135 140
 Lys Leu Asp Glu Ile Cys Gln Ala Ser Phe Thr Ile Asn Ser Lys Ile
 145 150 155 160
 Ile Asn Tyr Ile Lys Gln Cys Val Ile Glu Glu Cys Asn Glu Ile Phe
 165 170 175
 Ser Ala Phe Glu Val Val Val Ala Leu Thr Trp Ile Ala Arg Thr Lys
 180 185 190
 Ala Phe Gln Ile Pro His Ser Glu Asn Val Met Met Leu Phe Gly Met
 195 200 205
 Asp Ala Arg Lys Tyr Phe Asn Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Ile Gly Thr Ser Cys Val Ile Glu Asn Val Gln Asp Leu Leu
 225 230 235 240
 Asn Gly Ser Leu Ser Arg Ala Val Met Ile Thr Lys Lys Ser Lys Val
 245 250 255
 Pro Leu Ile Glu Asn Leu Arg Ser Arg Ile Val Ala Asn Gln Ser Gly
 260 265 270
 Val Asp Glu Glu Ile Lys His Glu Asn Val Val Gly Phe Gly Asp Trp
 275 280 285
 Arg Arg Leu Gly Phe His Glu Val Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 25
 <211> 1320
 <212> DNA
 <213> *Taxus cuspidata*

<400> 25
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 cccaaaaata tctgcacct ctccccatt gacaacaaaa ctagaggact aaccaacata 120
 ttatcagtct acaatgcctc ccagagagtt tctgtttctg cagatcctgc aaaaacaatt 180
 cgagaggctc tctccaaggt gctggtttat tatccccctt ttgctggaag gctgagaaac 240
 acagaaaatg gggatcttga agtggagtg c acaggggagg gtgccgtctt tgtggaagcc 300
 atggcggaca acgaccttct agtattacaa gatttcaatg agtacgatcc atcatttcag 360
 cagctagttt ttaatcttcg agaggatgac aatattgagg acctccatct tctaactgtt 420
 caggtaactc gttttacatg tggaggattt gttgtgggca caagattcca ccatagtgtg 480
 tctgatggaa aaggaatcgg ccagttactt aaaggcatgg gagagatggc aaggggggag 540
 tttaagccct cgttagaacc aatatggaat agagaaatgg tgaagcctga agacattatg 600
 tacctccagt ttgatcactt tgatttcata caccacctc ttaatcttga gaagtctatt 660
 caagcatcta tggtataaag ctttgagaga ataaattata tcaaacgatg catgatggaa 720
 gaatgcaaag aatttttttc tgcatttgaa gttgtagtag cattgatttg gctggcaagg 780
 acaaagtctt ttcgaattcc acccaatgag tatgtgaaaa ttatctttcc aatcgacatg 840

aggaattcat ttgactcccc tcttccaaag ggataactatg gtaatgctat tggtaatgca 900
 tgtgcaatgg ataatgtcaa agacctctta aatggatctc ttttatatgc tctaattgctt 960
 ataaaagaaat caaagtttgc tttaaatgag aatttcaa atcaagaatctt gacaaaacca 1020
 tctacattag atgcgaatat gaagcatgaa aatgtagtcg gatgtggcga ttggaggaat 1080
 ttgggatttt atgaagcaga ttttggatgg ggaaatgcag tgaatgtaag ccccatgcag 1140
 caacaaagag agcatgaatt agctatgcaa aattattttc tttttctccg atcagctaag 1200
 aacatgattg atggaatcaa gataactaatg ttcatgcctg catcaatggt gaaaccattc 1260
 aaaattgaaa tggaagtcac aataaaca aaatattgta ctctaagtta 1320

<210> 26

<211> 440

<212> PRT

<213> Taxus cuspidata

<400> 26

Met Gly Arg Phe Asn Val Asp Met Ile Glu Arg Val Ile Val Ala Pro
 1 5 10 15

Cys Leu Gln Ser Pro Lys Asn Ile Leu His Leu Ser Pro Ile Asp Asn
 20 25 30

Lys Thr Arg Gly Leu Thr Asn Ile Leu Ser Val Tyr Asn Ala Ser Gln
 35 40 45

Arg Val Ser Val Ser Ala Asp Pro Ala Lys Thr Ile Arg Glu Ala Leu
 50 55 60

Ser Lys Val Leu Val Tyr Tyr Pro Pro Phe Ala Gly Arg Leu Arg Asn
 65 70 75 80

Thr Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly Glu Gly Ala Val
 85 90 95

Phe Val Glu Ala Met Ala Asp Asn Asp Leu Ser Val Leu Gln Asp Phe
 100 105 110

Asn Glu Tyr Asp Pro Ser Phe Gln Gln Leu Val Phe Asn Leu Arg Glu
 115 120 125

Asp Val Asn Ile Glu Asp Leu His Leu Leu Thr Val Gln Val Thr Arg
 130 135 140

Phe Thr Cys Gly Gly Phe Val Val Gly Thr Arg Phe His His Ser Val
 145 150 155 160

Ser Asp Gly Lys Gly Ile Gly Gln Leu Leu Lys Gly Met Gly Glu Met
 165 170 175

Ala Arg Gly Glu Phe Lys Pro Ser Leu Glu Pro Ile Trp Asn Arg Glu
 180 185 190

Met Val Lys Pro Glu Asp Ile Met Tyr Leu Gln Phe Asp His Phe Asp
 195 200 205

Phe Ile His Pro Pro Leu Asn Leu Glu Lys Ser Ile Gln Ala Ser Met
 210 215 220

Val Ile Ser Phe Glu Arg Ile Asn Tyr Ile Lys Arg Cys Met Met Glu
 225 230 235 240

Glu Cys Lys Glu Phe Phe Ser Ala Phe Glu Val Val Val Ala Leu Ile

245	250	255
Trp Leu Ala Arg Thr Lys Ser Phe	Arg Ile Pro Pro Asn Glu Tyr Val	
260	265	270
Lys Ile Ile Phe Pro Ile Asp Met	Arg Asn Ser Phe Asp Ser Pro Leu	
275	280	285
Pro Lys Gly Tyr Tyr Gly Asn Ala	Ile Gly Asn Ala Cys Ala Met Asp	
290	295	300
Asn Val Lys Asp Leu Leu Asn Gly	Ser Leu Leu Tyr Ala Leu Met Leu	
305	310	315
Ile Lys Lys Ser Lys Phe Ala Leu	Asn Glu Asn Phe Lys Ser Arg Ile	
325	330	335
Leu Thr Lys Pro Ser Thr Leu Asp	Ala Asn Met Lys His Glu Asn Val	
340	345	350
Val Gly Cys Gly Asp Trp Arg Asn	Leu Gly Phe Tyr Glu Ala Asp Phe	
355	360	365
Gly Trp Gly Asn Ala Val Asn Val	Ser Pro Met Gln Gln Gln Arg Glu	
370	375	380
His Glu Leu Ala Met Gln Asn Tyr	Phe Leu Phe Leu Arg Ser Ala Lys	
385	390	395
Asn Met Ile Asp Gly Ile Lys Ile	Leu Met Phe Met Pro Ala Ser Met	
405	410	415
Val Lys Pro Phe Lys Ile Glu Met	Glu Val Thr Ile Asn Lys Tyr Val	
420	425	430
Ala Lys Ile Cys Asn Ser Lys Leu		
435	440	

<210> 27
 <211> 1317
 <212> DNA
 <213> Taxus cuspidata

<400> 27
 atggagaaga cagattttaca cgtaaactctg attgagaaag tgatgggttg gccatccccg 60
 cctctgcccc aaaccaccct gcaactctcc tccatagaca acctgccagg ggtaagagga 120
 agcattttca atgccttggt aattttacaat gcctctccct ctcccaccat gatctctgca 180
 gatcctgcaa aaccaattag agaagctctc gccaaagatcc tgggtttatta tccccctttt 240
 gctggggcgcc tcagagagac agaaaatggg gatctggaag tgggaatgcac aggggagggg 300
 gctatgtttt tggaagccat ggcagacaat gagctgtctg tgttgggaga ttttgatgac 360
 agcaatccat catttcagca gctacttttt tcgcttccac tcgataccaa tttcaaagac 420
 ctctctcttc tgggtgtttc ggtaactcgt tttacatgtg gaggctttgt tgttggagt 480
 agtttccacc atggtgtatg tgatgggtcga ggagcggccc aatttcttaa aggtttggca 540
 gagatggcac ggggagaggt taagctctca ttggaaccaa tatggaatag ggaactagt 600
 aagcttgatg accctaaata ctttcaattt tttcactttg aattcctacg agcgccttca 660
 attgttgaga aaattgttca aacatatttt attatagatt ttgagaccat aaattatata 720
 aaacaatctg ttatggaaga atgtaaagaa ttttgctctt cattcgaagt tgcatacagca 780
 atgacttgga tagcaaggac aagagctttt caaattccag aaagtgaagta cgtgaaaatt 840
 ctcttcgga tggacatgag gaactcattt aatccccctc ttccaagcgg atactatgg 900
 aactccattg gtaccgcatg tgcagtggat aatgttcaag acctcttaag tggatctctt 960

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ttgcgtgcta taatgattat aaagaaatca aaggtctctt taaatgataa tttcaagtca 1020
agagctgtgg tgaagccatc tgaattggat gtgaatatga atcatgaaaa cgtagttgca 1080
tttgctgatt ggagccgatt gggatttgat gaagtggatt ttggttgggg gaatgcggtg 1140
agtgtaaagc ctgtgcaaca acagtctgcg ttagcaatgc aaaattattt tcttttccta 1200
aaaccttcca agaacaagcc cgatggaatc aaaatattaa tgtttctgcc cctatcaaaa 1260
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```

<210> 28

<211> 439

<212> PRT

<213> Artificial Sequence

<400> 28

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Met Glu Lys Thr Asp Leu His Val Asn Leu Ile Glu Lys Val Met Val
  1              5              10              15

```

```

Gly Pro Ser Pro Pro Leu Pro Lys Thr Thr Leu Gln Leu Ser Ser Ile
          20              25              30

```

```

Asp Asn Leu Pro Gly Val Arg Gly Ser Ile Phe Asn Ala Leu Leu Ile
          35              40              45

```

```

Tyr Asn Ala Ser Pro Ser Pro Thr Met Ile Ser Ala Asp Pro Ala Lys
          50              55              60

```

```

Pro Ile Arg Glu Ala Leu Ala Lys Ile Leu Val Tyr Tyr Pro Pro Phe
          65              70              75              80

```

```

Ala Gly Arg Leu Arg Glu Thr Glu Asn Gly Asp Leu Glu Val Glu Cys
          85              90              95

```

```

Thr Gly Glu Gly Ala Met Phe Leu Glu Ala Met Ala Asp Asn Glu Leu
          100             105             110

```

```

Ser Val Leu Gly Asp Phe Asp Asp Ser Asn Pro Ser Phe Gln Gln Leu
          115             120             125

```

```

Leu Phe Ser Leu Pro Leu Asp Thr Asn Phe Lys Asp Leu Ser Leu Leu
          130             135             140

```

```

Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val
          145             150             155             160

```

```

Ser Phe His His Gly Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Leu
          165             170             175

```

```

Lys Gly Leu Ala Glu Met Ala Arg Gly Glu Val Lys Leu Ser Leu Glu
          180             185             190

```

```

Pro Ile Trp Asn Arg Glu Leu Val Lys Leu Asp Asp Pro Lys Tyr Leu
          195             200             205

```

```

Gln Phe Phe His Phe Glu Phe Leu Arg Ala Pro Ser Ile Val Glu Lys
          210             215             220

```

```

Ile Val Gln Thr Tyr Phe Ile Ile Asp Phe Glu Thr Ile Asn Tyr Ile
          225             230             235             240

```

```

Lys Gln Ser Val Met Glu Glu Cys Lys Glu Phe Cys Ser Ser Phe Glu
          245             250             255

```

Val Ala Ser Ala Met Thr Trp Ile Ala Arg Thr Arg Ala Phe Gln Ile
 260 265 270
 Pro Glu Ser Glu Tyr Val Lys Ile Leu Phe Gly Met Asp Met Arg Asn
 275 280 285
 Ser Phe Asn Pro Pro Leu Pro Ser Gly Tyr Tyr Gly Asn Ser Ile Gly
 290 295 300
 Thr Ala Cys Ala Val Asp Asn Val Gln Asp Leu Leu Ser Gly Ser Leu
 305 310 315 320
 Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Val Ser Leu Asn Asp
 325 330 335
 Asn Phe Lys Ser Arg Ala Val Val Lys Pro Ser Glu Leu Asp Val Asn
 340 345 350
 Met Asn His Glu Asn Val Val Ala Phe Ala Asp Trp Ser Arg Leu Gly
 355 360 365
 Phe Asp Glu Val Asp Phe Gly Trp Gly Asn Ala Val Ser Val Ser Pro
 370 375 380
 Val Gln Gln Gln Ser Ala Leu Ala Met Gln Asn Tyr Phe Leu Phe Leu
 385 390 395 400
 Lys Pro Ser Lys Asn Lys Pro Asp Gly Ile Lys Ile Leu Met Phe Leu
 405 410 415
 Pro Leu Ser Lys Met Lys Ser Phe Lys Ile Glu Met Glu Ala Met Met
 420 425 430
 Lys Lys Tyr Val Ala Lys Val
 435

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:proteolytic
fragment

<400> 29

Thr Thr Leu Gln Leu Ser Ser Ile Asp Asn Leu Pro Gly Val Arg
 1 5 10 15

<210> 30

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:proteolytic
fragment

<400> 30

Ile Leu Val Tyr Tyr Pro Pro Phe Ala Gly Arg
1 5 10

<210> 31
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:proteolytic
fragment

<400> 31
Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
1 5 10

<210> 32
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:proteolytic
fragment

<400> 32
Lys Gly Leu Ala Glu Ile Ala Arg Gly Glu Val Lys
1 5 10

<210> 33
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:proteolytic
fragment

<400> 33
Asn Leu Pro Asn Asp Thr Asn Pro Ser Ser Gly Tyr Tyr Gly Asn
1 5 10 15

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 34
atnctngtnt attatccncc

20

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 35
tattatccnc cntttgcngg 20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 36
ttctatccnt tcgcnggnag 20

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 37
tactatccnt tngcnggnag 20

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 38
ctaaaaccna ccccntttgg 20

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
sequence

<400> 39
Phe Tyr Pro Phe Ala Gly Arg
1 5

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus

sequence

<400> 40

Tyr Tyr Pro Leu Ala Gly Arg
1 5

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence

<400> 41

Asp Phe Gly Trp Gly Lys Pro
1 5

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 42

cctcatcttt cccccattga taat

24

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 43

aaaaagaaaa taattttgcc atgcaag

27

<210> 44

<211> 1320

<212> DNA

<213> Taxus cuspidata

<400> 44

atggcaggct caacagaatt tgttgtaaga agcttagaga gagtgatggt ggctccaagc 60
cagccatcgc ccaaagcttt cctgcagctc tccacccttg acaatctacc aggggtgaga 120
gaaaacattt ttaacacctt gttagtctac aatgcctcag acagagtttc cgtagatcct 180
gcaaaagtaa ttcggcaggc tctctccaag gtgttggtgt actattcccc ttttgagggg 240
cgtctcagga aaaaagaaaa tggagatctt gaagtggagt gcacagggga ggggtgctctg 300
tttgtggaag ccatggctga cactgacctc tcagtcttag gagatttgga tgactacagt 360
ccttcacttg agcaactact tttttgtctt ccgcctgata cagatattga ggacatccat 420
cctctgggtg ttcaggtaac tcgttttaca tgtggagggt ttgttgtagg ggtgagtttc 480
tgccatggta tatgtgatgg actaggagca ggccagtttc ttatagccat gggagagatg 540
gcaaggggag agattaagcc ctctcggag ccaatatgga agagagaatt gctgaagccg 600
gaagaccctt tataccggtt ccagtattat cactttcaat tgatttgccc gccttcaaca 660
ttcgggaaaa tagttcaagg atctcttggt ataacctctg agacaataaa ttgtatcaaa 720

caatgcctta gggaagaaag taaagaattt tgctctgcgt tcgaagttgt atctgcattg 780
 gcttggatag caaggacaag ggctcttcaa attccacata gtgagaatgt gaagcttatt 840
 tttgcaatgg acatgagaaa attattttaat ccaccacttt cgaagggata ctacggtaat 900
 tttgttggtt ccgtatgtgc aatggataat gtcaaggacc tattaagtgg atctctttttg 960
 cgtgttgtaa ggattataaa gaaagcaaag gtctctttaa atgagcattt cacgtcaaca 1020
 atcgtgacac cccgttctgg atcagatgag agtatcaatt atgaaaacat agttggattt 1080
 ggtgatcgaa ggcgattggg atttgatgaa gtagactttg ggtgggggca tgcagataat 1140
 gtaagtctcg tgcaacatgg attgaaggat gtttcagtcg tgcaaagtta ttttcttttc 1200
 atacgacctc ccaagaataa ccccgatgga atcaagatcc tatcgttcat gccccgtca 1260
 atagtgaat ccttcaaatt tgaaatggaa accatgacaa acaaatatgt aactaagcct 1320

<210> 45

<211> 440

<212> PRT

<213> *Taxus cuspidata*

<400> 45

Met Ala Gly Ser Thr Glu Phe Val Val Arg Ser Leu Glu Arg Val Met
 1 5 10 15

Val Ala Pro Ser Gln Pro Ser Pro Lys Ala Phe Leu Gln Leu Ser Thr
 20 25 30

Leu Asp Asn Leu Pro Gly Val Arg Glu Asn Ile Phe Asn Thr Leu Leu
 35 40 45

Val Tyr Asn Ala Ser Asp Arg Val Ser Val Asp Pro Ala Lys Val Ile
 50 55 60

Arg Gln Ala Leu Ser Lys Val Leu Val Tyr Tyr Ser Pro Phe Ala Gly
 65 70 75 80

Arg Leu Arg Lys Lys Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly
 85 90 95

Glu Gly Ala Leu Phe Val Glu Ala Met Ala Asp Thr Asp Leu Ser Val
 100 105 110

Leu Gly Asp Leu Asp Asp Tyr Ser Pro Ser Leu Glu Gln Leu Leu Phe
 115 120 125

Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp Ile His Pro Leu Val Val
 130 135 140

Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
 145 150 155 160

Cys His Gly Ile Cys Asp Gly Leu Gly Ala Gly Gln Phe Leu Ile Ala
 165 170 175

Met Gly Glu Met Ala Arg Gly Glu Ile Lys Pro Ser Ser Glu Pro Ile
 180 185 190

Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp Pro Leu Tyr Arg Phe Gln
 195 200 205

Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro Ser Thr Phe Gly Lys Ile
 210 215 220

Val Gln Gly Ser Leu Val Ile Thr Ser Glu Thr Ile Asn Cys Ile Lys
 225 230 235 240

Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe Cys Ser Ala Phe Glu Val
 245 250 255
 Val Ser Ala Leu Ala Trp Ile Ala Arg Thr Arg Ala Leu Gln Ile Pro
 260 265 270
 His Ser Glu Asn Val Lys Leu Ile Phe Ala Met Asp Met Arg Lys Leu
 275 280 285
 Phe Asn Pro Pro Leu Ser Lys Gly Tyr Tyr Gly Asn Phe Val Gly Thr
 290 295 300
 Val Cys Ala Met Asp Asn Val Lys Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320
 Arg Val Val Arg Ile Ile Lys Lys Ala Lys Val Ser Leu Asn Glu His
 325 330 335
 Phe Thr Ser Thr Ile Val Thr Pro Arg Ser Gly Ser Asp Glu Ser Ile
 340 345 350
 Asn Tyr Glu Asn Ile Val Gly Phe Gly Asp Arg Arg Arg Leu Gly Phe
 355 360 365
 Asp Glu Val Asp Phe Gly Trp Gly His Ala Asp Asn Val Ser Leu Val
 370 375 380
 Gln His Gly Leu Lys Asp Val Ser Val Val Gln Ser Tyr Phe Leu Phe
 385 390 395 400
 Ile Arg Pro Pro Lys Asn Asn Pro Asp Gly Ile Lys Ile Leu Ser Phe
 405 410 415
 Met Pro Pro Ser Ile Val Lys Ser Phe Lys Phe Glu Met Glu Thr Met
 420 425 430
 Thr Asn Lys Tyr Val Thr Lys Pro
 435 440

<210> 46

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 46

gggaattcca tatggcaggc tcaacagaat ttgtgg

36

<210> 47

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 47

gtttatacat tgattcggaa ctagatctga tc

32

<210> 48

<211> 6 ..

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 amino acid motif found in acyl transferases

<220>

<221> VARIANT

<222> (2)..(4)

<223> Any amino acid

<400> 48

His Xaa Xaa Xaa Asp Gly
1 5

<210> 49

<211> 1332

<212> DNA

<213> Taxus cuspidata

<400> 49

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ccatgccagc cgacgcccac aacaatcctg cagctctcta gcattgacaa aatgggagga 120
ggatttgcca acgtattgct agtcttcggt gcctcccatg gcgtttctgc agatcctgca 180
aaaacaattc gagaggctct ctccaagacc ttgggtctttt atttcccttt tgctgggcgg 240
ctcagaaaaga aagaagatgg ggatatcgaa gtggagtgca tagagcaggg agctctgttc 300
gtggaagcca tggcgggacaa cgatctttca ctggatacag attacaagga cctccatctt 420
ttatttcggc agctacaatc ttcgctttca ctggatacag attacaagga cctccatctt 420
atgactgttc aggttaactcc gtttacatgt ggggggtttg tcatgggaac gagtgtacac 480
caaagtatat gcgatggaaa tggattgggg caatttttta aaagcatggc agagatagtg 540
aggggagaag ttaagccctc aatcgaacca atatggaata gagaattggt gaagcctgaa 600
gactatatac acctccagtt gtatgtcagt gaattcattc gccaccttt agtagttgag 660
aaagttgggc aaacatctct tgttataagc ttcgagaaaa taaatcatat caaacgatgc 720
attatggaag aaagtaaaga atctttctct tcatttgaaa ttgtaacagc aatggttttg 780
ctagcaagga caagggcttt tcaaattcca cacaacgagg atgtgactct tctccttgca 840
atggatgcaa ggagatcatt tgacccccc attccgaagg gatactacgg taatgtcatt 900
gtactacat atgcaaaaaga taatgtccac aacctcttaa gtggatctct tttgcatgct 960
ctaacagtta taaagaaatc aatgtcctca ttttatgaga atatgacctc aagagtcttg 1020
gtgaacccat ctacattaga tttgagtatg aagtatgaaa atgtagtttc acttagtgat 1080
tggagccggg tgggacataa tgaagtggac tttgggtggg gaaatgcaat aaatgtaagc 1140
actctgcaac aacaatggga aaatgaggtg gctataccaa ctttttttac tttccttcaa 1200
actcccaaga atataccaga tggaatcaag atactaatgt tcatgcccc atcaagagag 1260
aaaacattcg aaattgaagt ggaagccatg ataagaaaat atttgactaa agtgtcgcag 1320
tcaaagctat aa
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<210> 50

<211> 443

<212> PRT

<213> Taxus cuspidata

<400> 50

Met Glu Lys Ser Gly Ser Ala Asp Leu His Val Asn Ile Ile Glu Arg
1 5 10 15

Val Val Val Ala Pro Cys Gln Pro Thr Pro Lys Thr Ile Leu Gln Leu

20					25					30					
Ser	Ser	Ile	Asp	Lys	Met	Gly	Gly	Gly	Phe	Ala	Asn	Val	Leu	Leu	Val
35					40					45					
Phe	Gly	Ala	Ser	His	Gly	Val	Ser	Ala	Asp	Pro	Ala	Lys	Thr	Ile	Arg
50				55				60							
Glu	Ala	Leu	Ser	Lys	Thr	Leu	Val	Phe	Tyr	Phe	Pro	Phe	Ala	Gly	Arg
65				70				75						80	
Leu	Arg	Lys	Lys	Glu	Asp	Gly	Asp	Ile	Glu	Val	Glu	Cys	Ile	Glu	Gln
				85				90						95	
Gly	Ala	Leu	Phe	Val	Glu	Ala	Met	Ala	Asp	Asn	Asp	Leu	Ser	Val	Val
		100						105						110	
Arg	Asp	Leu	Asp	Glu	Tyr	Asn	Pro	Leu	Phe	Arg	Gln	Leu	Gln	Ser	Ser
		115						120						125	
Leu	Ser	Leu	Asp	Thr	Asp	Tyr	Lys	Asp	Leu	His	Leu	Met	Thr	Val	Gln
130						135						140			
Val	Thr	Pro	Phe	Thr	Cys	Gly	Gly	Phe	Val	Met	Gly	Thr	Ser	Val	His
145				150						155				160	
Gln	Ser	Ile	Cys	Asp	Gly	Asn	Gly	Leu	Gly	Gln	Phe	Phe	Lys	Ser	Met
				165				170						175	
Ala	Glu	Ile	Val	Arg	Gly	Glu	Val	Lys	Pro	Ser	Ile	Glu	Pro	Ile	Trp
		180						185						190	
Asn	Arg	Glu	Leu	Val	Lys	Pro	Glu	Asp	Tyr	Ile	His	Leu	Gln	Leu	Tyr
		195						200						205	
Val	Ser	Glu	Phe	Ile	Arg	Pro	Pro	Leu	Val	Val	Glu	Lys	Val	Gly	Gln
210						215						220			
Thr	Ser	Leu	Val	Ile	Ser	Phe	Glu	Lys	Ile	Asn	His	Ile	Lys	Arg	Cys
225				230						235				240	
Ile	Met	Glu	Glu	Ser	Lys	Glu	Ser	Phe	Ser	Ser	Phe	Glu	Ile	Val	Thr
				245				250						255	
Ala	Met	Val	Trp	Leu	Ala	Arg	Thr	Arg	Ala	Phe	Gln	Ile	Pro	His	Asn
		260						265						270	
Glu	Asp	Val	Thr	Leu	Leu	Leu	Ala	Met	Asp	Ala	Arg	Arg	Ser	Phe	Asp
		275				280						285			
Pro	Pro	Ile	Pro	Lys	Gly	Tyr	Tyr	Gly	Asn	Val	Ile	Gly	Thr	Thr	Tyr
290						295						300			
Ala	Lys	Asp	Asn	Val	His	Asn	Leu	Leu	Ser	Gly	Ser	Leu	Leu	His	Ala
305				310						315				320	
Leu	Thr	Val	Ile	Lys	Lys	Ser	Met	Ser	Ser	Phe	Tyr	Glu	Asn	Met	Thr
				325				330						335	
Ser	Arg	Val	Leu	Val	Asn	Pro	Ser	Thr	Leu	Asp	Leu	Ser	Met	Lys	Tyr
		340						345						350	

Glu Asn Val Val Ser Leu Ser Asp Trp Ser Arg Leu Gly His Asn Glu
355 360 365

Val Asp Phe Gly Trp Gly Asn Ala Ile Asn Val Ser Thr Leu Gln Gln
370 375 380

Gln Trp Glu Asn Glu Val Ala Ile Pro Thr Phe Phe Thr Phe Leu Gln
385 390 395 400

Thr Pro Lys Asn Ile Pro Asp Gly Ile Lys Ile Leu Met Phe Met Pro
405 410 415

Pro Ser Arg Glu Lys Thr Phe Glu Ile Glu Val Glu Ala Met Ile Arg
420 425 430

Lys Tyr Leu Thr Lys Val Ser His Ser Lys Leu
435 440

<210> 51
<211> 1338
<212> DNA
<213> *Taxus cuspidata*

<400> 51
atgaagaaga cagggttcggt tgcagagttc catgtgaata tgattgagcg agtcatgggtg 60
agaccgtgcc tgccttcgcc caaaacaatc ctccctctct ccgccattga caacatggca 120
agagcttttt ctaacgtatt gctggtctac gctgccaca tggacagagt ctctgcagat 180
cctgcaaaag tgattcgaga ggctctctcc aagggtgctgg tttattatta cccttttgct 240
gggcggtcca gaaataaaga aaatggggaa cttgaagtgg agtgcacagg gcagggtggt 300
ctgtttctgg aagccatggc tgacagcgac ctttcagtct taacagatct ggataactac 360
aatccatcgt ttcagcagtt gattttttct ctaccacagg atacagatat tgaggacctc 420
catctcttga ttgttcaggt aactcgtttt acatgtgggg gttttgtgtt gggagcgaat 480
gtgtatggta gtgcattgca tgcaaaagga tttggccagt ttcttcaaag tatggcagag 540
atggcgagag gagagggttaa gccctcgatt gaaccgatat ggaatagaga actggtgaag 600
ctagaacatt gtatgccctt ccggatgagt catcttcaaa ttatacatgc acctgtaatt 660
gaggagaaat ttgttcaaac atctcttggt ataaactttg agataataaa tcatatcaga 720
cgacgcatca tggagaagac caaagaaagt ttatcttcat ttgaaattgt agcagcattg 780
gtttggctag caaagataaa ggcttttcaa attccacata gtgagaatgt gaagcttctt 840
tttgcaatgg acttgaggag atcatttaat cccctcttc cacatggata ctatggcaat 900
gcctttggta ttgcatgtgc aatggataat gtccatgacc ttctaagtgg atctcttttg 960
cgactataaa tgatcataaa gaaatcaaa ttctctttac acaaagaact caactcaaaa 1020
accgtgatga gctcatctgt agtagatgtc aatacgaagt ttgaagatgt agtttcaatt 1080
agtgattgga ggcattctat atattatgaa gtggactttg ggtggggaga tgcaatgaac 1140
gtgagcacta tgctacaaca acaggagcac gagaaatctc tgccaactta tttttctttc 1200
ctacaatcta ctaagaacat gccagatgga atcaagatgc taatgtttat gcctccatca 1260
aaactgaaaa aattcaaaat tgaaatagaa gctatgataa aaaaatatgt gactaaaagt 1320
tgtccgtcaa agttatga 1338

<210> 52
<211> 445
<212> PRT
<213> *Taxus cuspidata*

<400> 52
Met Lys Lys Thr Gly Ser Phe Ala Glu Phe His Val Asn Met Ile Glu
1 5 10 15

Arg Val Met Val Arg Pro Cys Leu Pro Ser Pro Lys Thr Ile Leu Pro
20 25 30

Leu Ser Ala Ile Asp Asn Met Ala Arg Ala Phe Ser Asn Val Leu Leu
 35 40 45
 Val Tyr Ala Ala Asn Met Asp Arg Val Ser Ala Asp Pro Ala Lys Val
 50 55 60
 Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Tyr Pro Phe Ala
 65 70 75 80
 Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95
 Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala Asp Ser Asp Leu Ser
 100 105 110
 Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser Phe Gln Gln Leu Ile
 115 120 125
 Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp Leu His Leu Leu Ile
 130 135 140
 Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Ala Asn
 145 150 155 160
 Val Tyr Gly Ser Ala Cys Asp Ala Lys Gly Phe Gly Gln Phe Leu Gln
 165 170 175
 Ser Met Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Ile Glu Pro
 180 185 190
 Ile Trp Asn Arg Glu Leu Val Lys Leu Glu His Cys Met Pro Phe Arg
 195 200 205
 Met Ser His Leu Gln Ile Ile His Ala Pro Val Ile Glu Glu Lys Phe
 210 215 220
 Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile Ile Asn His Ile Arg
 225 230 235 240
 Arg Arg Ile Met Glu Glu Arg Lys Glu Ser Leu Ser Ser Phe Glu Ile
 245 250 255
 Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys Ala Phe Gln Ile Pro
 260 265 270
 His Ser Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Arg Ser
 275 280 285
 Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly Asn Ala Phe Gly Ile
 290 295 300
 Ala Cys Ala Met Asp Asn Val His Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320
 Arg Thr Ile Met Ile Ile Lys Lys Ser Lys Phe Ser Leu His Lys Glu
 325 330 335
 Leu Asn Ser Lys Thr Val Met Ser Ser Val Val Asp Val Asn Thr
 340 345 350

Lys Phe Glu Asp Val Val Ser Ile Ser Asp Trp Arg His Ser Ile Tyr
 355 360 365
 Tyr Glu Val Asp Phe Gly Trp Gly Asp Ala Met Asn Val Ser Thr Met
 370 375 380
 Leu Gln Gln Gln Glu His Glu Lys Ser Leu Pro Thr Tyr Phe Ser Phe
 385 390 395 400
 Leu Gln Ser Thr Lys Asn Met Pro Asp Gly Ile Lys Met Leu Met Phe
 405 410 415
 Met Pro Pro Ser Lys Leu Lys Lys Phe Lys Ile Glu Ile Glu Ala Met
 420 425 430
 Ile Lys Lys Tyr Val Thr Lys Val Cys Pro Ser Lys Leu
 435 440 445

<210> 53
 <211> 1326
 <212> DNA
 <213> *Taxus cuspidata*

<400> 53
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 cctgtaaaaa taattagaga ggctctctcc aagggtgttg tgtattattt ccctcttgct 240
 gggcggtcca gaagtaaaga aattggggaa cttgaagtgg agtgcacagg ggatgggtgct 300
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 aatccatcat ttcagcagtt agtttttttg catccattgg acaactgctat tgaggatctt 420
 catcttgtga ttgttcaggt aacacgtttt acatgtgggg gcattgccgt tggagtgact 480
 ttgccccata gtgtatgtga tggacgtgga gcagcccagt ttgttacagc actggcagag 540
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 cctgaagacc ctctacatct ccagttaaat caatttgatt cgatatgccc acctccaatg 660
 ctggaggaat tgggtcaagc ttctttgtt ataaacgttg acaccataga atatatgaag 720
 caatgtgtca tggaggaatg taatgaattt tgttcgtctt ttgaagtagt ggcagcattg 780
 gtttgatag caccgacaaa ggctcttcaa attccacata ctgagaatgt gaagcttctc 840
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 gccattggta ctgcatatgc aatggataat gtccaagacc tcttaaattg atctcttttg 960
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 agggtagtta caaaccataa ttcattagat gtgaacaaga aatccgacaa cattcttgca 1080
 ttgagtgact ggaggcggtt gggattttat gaagccgatt ttgggtgggg aggtccactg 1140
 aatgtaagtt ccctgcaacg gttggaaaat ggattgccta tgtttagtag ttttctatac 1200
 ctactacctg ccaaaaacaa gtctgatgga atcaagctgc tactgtcttg tatgccacca 1260
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 gtgtga 1326

<210> 54
 <211> 441
 <212> PRT
 <213> *Taxus cuspidata*

<400> 54
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 Val Met Val Ala Pro Ser Leu Pro Ser Pro Lys Ala Thr Val Gln Leu
 20 25 30

Ser Val Val Asp Ser Leu Thr Ile Cys Arg Gly Ile Phe Asn Thr Leu
 35 40 45
 Leu Val Phe Asn Ala Pro Asp Asn Ile Ser Ala Asp Pro Val Lys Ile
 50 55 60
 Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Phe Pro Leu Ala
 65 70 75 80
 Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95
 Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val Glu Asp Thr Ile Ser
 100 105 110
 Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser Phe Gln Gln Leu Val
 115 120 125
 Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp Leu His Leu Val Ile
 130 135 140
 Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile Ala Val Gly Val Thr
 145 150 155 160
 Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Val Thr
 165 170 175
 Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Leu Glu Pro
 180 185 190
 Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp Pro Leu His Leu Gln
 195 200 205
 Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro Met Leu Glu Glu Leu
 210 215 220
 Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr Ile Glu Tyr Met Lys
 225 230 235 240
 Gln Cys Val Met Glu Glu Cys Asn Glu Phe Cys Ser Ser Phe Glu Val
 245 250 255
 Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys Ala Leu Gln Ile Pro
 260 265 270
 His Thr Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Lys Leu
 275 280 285
 Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly Asn Ala Ile Gly Thr
 290 295 300
 Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu Asn Gly Ser Leu Leu
 305 310 315 320
 Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala Asp Leu Lys Asp Asn
 325 330 335
 Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Tyr Ser Leu Asp Val Asn
 340 345 350
 Lys Lys Ser Asp Asn Ile Leu Ala Leu Ser Asp Trp Arg Arg Leu Gly

355

360

365

Phe Tyr Glu Ala Asp Phe Gly Trp Gly Gly Pro Leu Asn Val Ser Ser
370 ... 375 380

Leu Gln Arg Leu Glu Asn Gly Leu Pro Met Phe Ser Thr Phe Leu Tyr
385 390 395 400

Leu Leu Pro Ala Lys Asn Lys Ser Asp Gly Ile Lys Leu Leu Leu Ser
405 410 415

Cys Met Pro Pro Thr Thr Leu Lys Ser Phe Lys Ile Val Met Glu Ala
420 425 430

Met Ile Glu Lys Tyr Val Ser Lys Val
435 440

<210> 55

<211> 1347

<212> DNA

<213> *Taxus cuspidata*

<400> 55

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gacagactgc cagggatgaa gtttgctact tttagcgccg tgtagtcta caatgccagc 180
tctcactcca tttttgcaaa tcttgacacag attattcggc aggctctctc caaggtgttg 240
cagtattatc ccgcttttgc cgggcgggac agacagaaaag aaaatgagga actggaagtg 300
gagtgacacag gggagggtgc gctgtttgtg gaagcccttg tgcacaatga tctttcagtc 360
ttgcgagatt tggatgcccc aaatgcatct tatgagcagt tgctcttttc gcttcgccc 420
aatatacagg ttcaggacct ccattcctctg attcttcagg taactcgttt tacgtgtgga 480
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ataactaatg tcatggatcc atcaagagtg aaattattca aagatgaaat ggaagccatg 1320
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<210> 56

<211> 448

<212> PRT

<213> *Taxus cuspidata*

<400> 56

Met Glu Lys Gly Asn Ala Ser Asp Val Pro Glu Leu His Val Gln Ile
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Cys Glu Arg Val Met Val Lys Pro Cys Val Pro Ser Pro Ser Pro Asn
20 25 30

Leu Val Leu Gln Leu Ser Ala Val Asp Arg Leu Pro Gly Met Lys Phe

35

40

45

Ala	Thr	Phe	Ser	Ala	Val	Leu	Val	Tyr	Asn	Ala	Ser	Ser	His	Ser	Ile
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Phe	Ala	Asn	Pro	Ala	Gln	Ile	Ile	Arg	Gln	Ala	Leu	Ser	Lys	Val	Leu
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Gln	Tyr	Tyr	Pro	Ala	Phe	Ala	Gly	Arg	Ile	Arg	Gln	Lys	Glu	Asn	Glu
				85					90					95	
Glu	Leu	Glu	Val	Glu	Cys	Thr	Gly	Glu	Gly	Ala	Leu	Phe	Val	Glu	Ala
			100					105					110		
Leu	Val	Asp	Asn	Asp	Leu	Ser	Val	Leu	Arg	Asp	Leu	Asp	Ala	Gln	Asn
		115					120					125			
Ala	Ser	Tyr	Glu	Gln	Leu	Leu	Phe	Ser	Leu	Pro	Pro	Asn	Ile	Gln	Val
	130					135						140			
Gln	Asp	Leu	His	Pro	Leu	Ile	Leu	Gln	Val	Thr	Arg	Phe	Thr	Cys	Gly
145					150					155					160
Gly	Phe	Val	Val	Gly	Val	Gly	Phe	His	His	Gly	Ile	Cys	Asp	Ala	Arg
				165					170					175	
Gly	Gly	Thr	Gln	Phe	Leu	Gln	Gly	Leu	Ala	Asp	Met	Ala	Arg	Gly	Glu
			180					185					190		
Thr	Lys	Pro	Leu	Val	Glu	Pro	Val	Trp	Asn	Arg	Glu	Leu	Ile	Lys	Pro
		195					200					205			
Glu	Asp	Leu	Met	His	Leu	Gln	Phe	His	Lys	Phe	Gly	Leu	Ile	Arg	Gln
	210					215					220				
Pro	Leu	Lys	Leu	Asp	Glu	Ile	Cys	Gln	Ala	Ser	Phe	Thr	Ile	Asn	Ser
225					230					235					240
Glu	Ile	Ile	Asn	Tyr	Ile	Lys	Gln	Cys	Val	Ile	Glu	Glu	Cys	Asn	Glu
			245						250					255	
Ile	Phe	Ser	Ala	Phe	Glu	Val	Val	Val	Ala	Leu	Thr	Trp	Ile	Ala	Arg
			260					265					270		
Thr	Lys	Ala	Phe	Gln	Ile	Pro	His	Asn	Glu	Asn	Val	Met	Met	Leu	Phe
		275					280					285			
Gly	Met	Asp	Ala	Arg	Lys	Tyr	Phe	Asn	Pro	Pro	Leu	Pro	Lys	Gly	Tyr
	290					295					300				
Tyr	Gly	Asn	Ala	Ile	Gly	Thr	Ser	Cys	Val	Ile	Glu	Asn	Val	Gln	Asp
305					310					315					320
Leu	Leu	Asn	Gly	Ser	Leu	Ser	Arg	Ala	Val	Met	Ile	Thr	Lys	Lys	Ser
				325					330					335	
Lys	Ile	Pro	Leu	Ile	Glu	Asn	Leu	Arg	Ser	Arg	Ile	Val	Ala	Asn	Gln
			340					345					350		
Ser	Gly	Val	Asp	Glu	Glu	Ile	Lys	His	Glu	Asn	Val	Val	Gly	Phe	Gly
		355					360					365			

Asp Trp Arg Arg Leu Gly Phe His Glu Val Asp Phe Gly Ser Gly Asp
 370 375 380

Ala Val Asn Ile Ser Pro Ile Gln Gln Arg Leu Glu Asp Asp Gln Leu
 385 390 395 400

Ala Met Arg Asn Tyr Phe Leu Phe Leu Arg Pro Tyr Lys Asp Met Pro
 405 410 415

Asn Gly Ile Lys Ile Leu Met Phe Met Asp Pro Ser Arg Val Lys Leu
 420 425 430

Phe Lys Asp Glu Met Glu Ala Met Ile Ile Lys Tyr Met Pro Lys Ala
 435 440 445

<210> 57
 <211> 1317
 <212> DNA
 <213> *Taxus cuspidata*

<400> 57
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 ttgttcgtct acgacagggg ttcaactggt tctgcaaadc ctgcaaaaac aattcgagag 180
 gctctctcca aggttttggg ttattattca ccttttgctg gaaggctcag aaacaaagaa 240
 aatggggatc ttgaagtgga gtgcagtggg gaggggtgctg tctttgtgga agccatggcg 300
 gacaacgagc ttccagtctt acaagatttg gatgagtact gtacatcgct taaacagcta 360
 atttttacag taccaatgga tacgaaaatt gaagacctcc atcttctaag tgttcaggta 420
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 ggaaaaggac tgggcccagtt tcttcaaggc atgagtgaga tttccaaggg agcattttaa 540
 ccctcactag aaccagtatg gaatagagaa atggtgaagc ctgaacacct tatgttcctc 600
 cagtttaata attttgaatt cgtaccacat cctcttaa at ttaagaagat tgttaaagca 660
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<210> 58
 <211> 438
 <212> PRT
 <213> *Taxus cuspidata*

<400> 58
 Met Glu Lys Leu His Val Asp Ile Ile Glu Arg Val Lys Val Ala Pro
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Cys Leu Pro Ser Ser Lys Glu Ile Leu Gln Leu Ser Ser Leu Asp Asn
 20 25 30

355

360

365

Gly Asn Leu Ser Asn Val Ile Pro Met Asp Gln Gln Ile Glu His Glu
370 --- 375 380

Ser Pro Val Gln Ser Arg Phe Met Leu Leu Arg Ser Ser Lys Asn Met
385 390 395 400

Gln Asn Gly Ile Lys Ile Leu Met Ser Met Pro Glu Ser Met Ala Lys
405 410 415

Pro Phe Lys Ser Glu Met Lys Phe Thr Ile Lys Lys Tyr Val Thr Gly
420 425 430

Ala Cys Phe Ser Glu Leu
435

[illegible]